

n Table : Universal

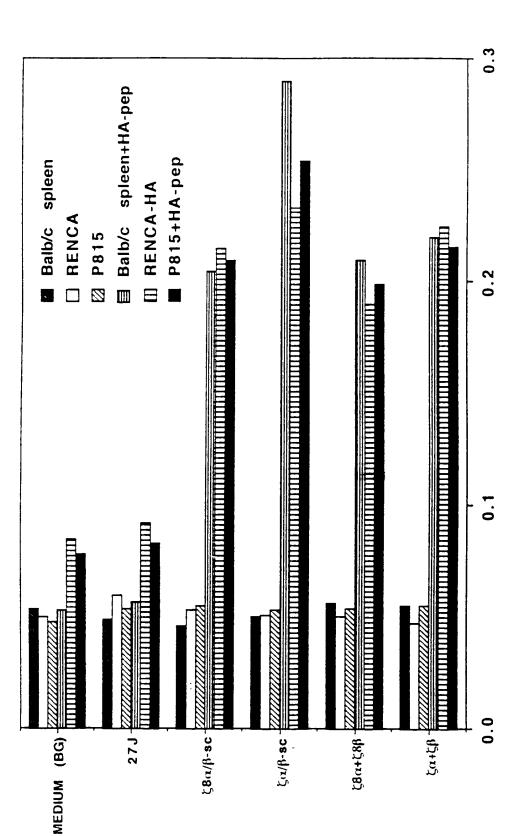
e: 1 - 1396 Mode: Normal

18 27 GAG ATG CAG AGG AAC CTG GGA GCT GTG CTG GGG ATT CTG TGG GTG CAG ATT --- --- --- --- --- --- --- --- ---A V L G I L Q R L G N 108 81 90 63 72 TGC TGG CTG AAA GAA CAG CAA GTG CAG CAG AGT CCC GCA TCC TTG GTT CTG CAG ... ... ... ... ... ... ... ... ... ... ... L K E Q Q V Q Q S P A S L V L 135 144 153 117 126 GAG GGG GAG AAC GCA GAG CTC CAG TGT AGC TTT TCC ATC TTT ACA AAC CAG GTG ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... EGENAELQCSFSIFT 0 198 171 189 180 CAG TGG TTT TAC CAA CGT CCT GGG GGA AGA CTC GTC AGC CTG TTG TAC AAT CCT ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... G R L V S L L Y N R P G Q 252 261 243 225 234 TCT GGG ACA AAG CAG AGT GGG AGA CTG ACA TCC ACA ACA GTC ATT AAA GAA CGT s T T V ĸ S G T K Q S G R L T 297 306 315 324 288 CGC AGC TOT TTG CAC ATT TOO TOO TOO CAG ATO ACA GAC TOA GGC ACT TAT CTO H I S S S Q I T D S G s s L 360 369 333 342 351 TGT GCC TCA AAT TCT GGA GGA AGC AAT GCA AAG CTA ACC TTC GGG AAA GGC ACT C A S N S G G S N A K L T F G K G 414 423 BOWHE 432 396 405 AAA CTC TCT GTT AAA TCA GGT GGC GGA GGG TCT GGC GGG GGT GGA TCC GGG GGT ... ... ... ... ... ... ... ... ... ... ... ... ... ... s v k s <u>g</u> g g G S G G G S G G LINKER 477 459 468 441 450 GGA GGC TCA GAG GCT GCA GTC ACC CAA AGC CCA AGA AAC AAG GTG GCA GTA ACA ... ... ... ... ... ... ... V A V T G G S E V T Q s P R N K A A 540 504 513 522 531 GGA GGA AAG GTG ACA TTG AGC TGT AAT CAG ACT AAT AAC CAC AAC AAC ATG TAC G G K V Ť L S C N Q T N N H 585 576 558 567 TGG TAT CGG CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC CAT TAT TCA TAT GGT ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... Y WYRQDTGHGLRLIH 639 612 621 630

GCT GGC AGC ACT GAG AAA GGA GAT ATC CCT GAT GGA TAC AAG GCC TCC AGA CCA ... ... ... ... ... ... ... ... ... ... ... ... ... ... ... A G S T E K G D I P D G Y K A S R P

FIGURE

200	711	557		700	666		\ mm	675			684			693					
:-		GAG												7.27				FIGURE 3B	
S	Q	E	N	P.	s	i.		L	Ξ	L	A	T	P	S		T	S	32	
		711			720			729			738			747			756	Û13	
GTG	TAC	TTC	TGT	GCC	AGC	GGT	GAG	ACA	GGG	ACC	AAC	GAA	AGA	TTA	TTT	TTC	GGT	<b>3</b>	
ν	Y	F	C	A	s	G	E	T	G	T	N	E	R	L	F	F	G		
CAT	GGA	765 ACC	AAG	CTG	774 TCT	GTC	CTG	7834 ACT	AGT	AAC	792 TCC	ATC	ATG	801 TAC	TTC	AGC	810 CAC		
н	G	Ť	K	L	S	V	L	T	s	N	s	I	М	Y	F	s	H		
mma	ama.	819	~~~		828			837			846			855			864	COO	
1110	GTG	CCG	GTC	TTC	CTG	CCA	GCG	AAG	ccc	ACC	ACG	ACG	CCA	GCG	CCG	CGA	CCA	CD8 HINGE	
F	v	P	v	F	L	P	A	K	P	T	Ţ	T	P	A	P	R	P		
		873			882			891			900			909			918		
CCA	ACA	CCG	GCG	ccc		ATC	GCG		CAG	ccc		TCC	CTG	CGC	CCA	TCT			
P		P	 А	P	 T	ī	Α	s	Q	 Р	L	s	L L	 R	p	s	s		
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	DGD.		220	* * * *	936	ma a	ma c	945	ame.	C N C	954	<b>N</b>	~~~	963	<b>N</b> m.c	m a m	972 CCT		
		GAT				1.60	TAC			GAT	GGA	ATC		1110	ATC	TAT	GGT		
S	R	D	P	K	L	C	Y	L	Ļ	D	G	I	L	F	I	Y	G		
14		981			990			999			1008			1017			1026		
GTC	ATT	crc	ACT	GCC		TTC	CTG		GTG			AGC		AGC	GCA				
v	I	L	 T	Α	L L	F	L	R.	v	к	F	s	R	s	Α	D	Α		
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ECC		.035 TAC	CAG		L044 GGC	CAG		.053	רידיר		L062	GAG		1071 מעב	∀ باست		CGA		
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P												_	Ļ	N		~	_		
	A	Y	Q	Q	G	Q	N	Q	L	Y	N	E	14	14	L	G	R	2 Chan	
		Y .089	Q		G 1098	Q		Q .107	L		711e N	£		1125	L		R 1134	2 Chain	
	I GAG	.089 GAG	TAC	I GAT	1098 GTT	TTG	I GAC	.107 AAG	AGA	CGT	GGC	CGG	GAC	1125 CCT	GAG	ATG	1134 GGG	2 Chain	
	GAG	.089 GAG	TAC	GAT	098 GTT	TTG	GAC	.107 AAG	AGA	CGT	GGC	CGG	GAC	1125 CCT	GAG	ATG	1134 GGG	2 Chair	
	GAG  E	.089 GAG  E	TAC	GAT D	098 GTT  V	TTG  L	GAC  D	107 AAG  K	AGA  R	CGT R	G GGC	CGG 	GAC D	CCT P	GAG  E	ATG 	GGG GG	2 Chair	
R R	GAG  E	.089 GAG  E	TAC	GAT D	098 GTT V	TTG	GAC D	.107 AAG  K	AGA R	CGT R	GGC G	CGG  R	GAC D	1125 CCT P	GAG  E	ATG  M	1134 GGG  G	2 Chair	
R GGA	GAG E E	.089 GAG E .143 CCG	TAC Y AGA	GAT D AGG	V L152 AAG	TTG L AAC	GAC D CCT	.107 AAG  K .161 CAG	AGA R GAA	CGT R R GGC	GGC GGC GGC GGC GGC	CGG R TAC	GAC D AAT	CCT P 1179 GAA	GAG E CTG	ATG M CAG	1134 GGG G G 1188 AAA	2 Chain	•
R GGA	GAG E E	.089 GAG  E .143 CCG	TAC Y AGA	GAT D AGG	V L152 AAG	TTG L AAC	GAC D CCT	.107 AAG  K .161 CAG	AGA R GAA	CGT R R GGC	GGC GGC GGC GGC GGC	CGG R TAC	GAC D AAT	CCT P 1179 GAA	GAG E CTG	ATG M CAG	1134 GGG G G 1188 AAA	2 Chair	
R GGA	GAG E AAG K	.089 GAG E .143 CCG	TAC Y AGA	GAT D D AGG	V L152 AAG	TTG L AAC	GAC D D CCT	.107 AAG  K .161 CAG	AGA R GAA	CGT R GGC	GGC GGC L170 CTG	CGG R TAC	GAC D AAT	CCT P 1179 GAA	GAG E CTG	ATG M CAG	1134 GGG  G 1188 AAA	2 Chain	•
R GGA GAT	GAG E AAG K AAG	.089 GAG E .143 CCG P	TAC Y AGA R	GAT D AGG R	098 GTT V 1152 AAG  K	TTG L AAC N TAC	GAC D CCT P AGT	.107 AAG  K .161 CAG 	AGA R GAA E	CGT R GGC	GGC GGC 170 CTG L	CGG R TAC	GAC D AAT	1125 CCT P 1179 GAA E	GAG E CTG	ATG M CAG	1134 GGG  G 1188 AAA  K	2 Chair	•
R GGA G	GAG E AAG K AAG	.089 GAG  E .143 CCG  P	TAC Y AGA R GCG	GAT D AGG R GAG	V L152 AAG K L206	TTG L AAC N TAC	GAC D CCT P AGT	L107 AAG K L161 CAG Q L215 GAG	AGA R GAA E	CGT R GGC	GGC GCTG CTG L	CGG R TAC	GAC D AAT N	1125 CCT P 1179 GAA E 1233 GAG	GAG E CTG	ATG M CAG	1134 GGG G 1188 AAA  K	2 Chain	•
R GGA G	GAG E AAG K AAG K	.089 GAG  E .143 CCG  P .197 ATG	TAC Y AGA R GCG	GAT D AGG R GAG E	V L152 AAG K L206 GCC	TTG L AAC N TAC	GAC D CCT P AGT	.107 AAG .161 CAG .215 GAG	AGA R GAA E ATT	CGT R GGC G	GGC GGC 170 CTG L L L224 ATG	CGG R TAC Y	GAC D AAT N GGC	1125 CCT P 1179 GAA  E 1233 GAG	GAG E CTG L CGC	ATG M CAG CGG	1134 GGG G 1188 AAA  K 1242 AGG	2 Chair	
R GGA GAT	GAG E AAG K AAG K	.089 GAG  E .143 CCG  P	TAC Y AGA R GCG	GAT D AGG R GAG E	V 152 AAG  K 1206 GCC  A	TTG L AAC N TAC	GAC D CCT P AGT	.107 AAG  K .161 CAG  Q .215 GAG	AGA R GAA E ATT	CGT R GGC G	116 GGC G 170 CTG L L 224 ATG	CGG R TAC Y	GAC D AAT N GGC	1125 CCT P 1179 GAA  E 1233 GAG	GAG E CTG L CGC	ATG M CAG CGG	1134 GGG G 1188 AAA  K 1242 AGG	2 Chair	
GGA GAT	GAG E AAG K AAG K AAG	.089 GAG  E .143 CCG  P .197 ATG  M	TAC Y  AGA R  GCG A  CAC	GAT  AGG  R  GAG  GAG  E  GAT	V 152 AAG  K 1206 GCC  A	TTG L AAC N TAC	GAC D CCT P AGT TAC	107 AAG K .161 CAG .215 GAG E	AGA R GAA E ATT	CGT R GGC G	GGC GGCTG CTG L L224 ATG M L276 AGT	CGG R TAC Y AAA K	GAC D AAT N GGC G	1125 CCT P 1179 GAA  E 1233 GAG  E	GAG E CTG L CGC	ATG M CAG Q CGG R	1134 GGG G 1188 AAA  K 1242 AGG  R	2 Chair	
GGA GAT	GAG E L AAG K AAG K AAG K	089 GAG E .143 CCG P .197 ATG  M	TAC Y AGA R GCG A CAC	GAT  AGG  R  GAG  GAG  E  GAT  D	V 152 AAG K 1206 GCC A GGC G	TTG L AAC N TAC Y CTT	GAC D CCT P AGT S TAC	107 AAG  K .161 CAG  Q .215 GAG  E	AGA R GAA E ATT I GGT	CGT R GGC G G G G G G	GGC GGC GTG L 170 CTG ATG ATG AGT	CGG R TAC Y AAA K ACA T	GAC D AAT N GGC G	1125 CCT P 1179 GAA  E 1233 GAG  E	GAG E CTG L CGC R	ATG M CAG CGG R	1134 GGG G 1188 AAA K 1242 AGG R 1296 ACC	2 Chair	
GGA GGC GGC G	GAG E AAG K AAG K AAG K AAG K	.089 GAG  E .143 CCG  P .197 ATG  M	TAC Y AGA R GCG A CAC	GAT D AGG R GAG E GAT D	V 152 AAG K 1206 GCC A 260 GGC G	TTG L AAC N TAC Y CTT	GAC D CCT P AGT TAC	107 AAG  K .161 CAG  Q .215 GAG  E	AGA R GAA E ATT I GGT	CGT R GGC G	GGC GGC CTG CTG ATG M AGT S S 1332	CGG R TAC Y AAA K ACA	GAC  AAT  N  GGC  GCC  A	1125 CCT P 1179 GAA  E 1233 GAG  E	GAG E CTG L CGC R AAG K	ATG M CAG Q CGGG R GAC	1134 GGG G 1188 AAA  K 1242 AGG  T	2 Chair	
GGA GGC GGC G	GAG E AAG K AAG K AAG K AAG K	.089 GAG  E .143 CCG  P .197 ATG  M	TAC Y AGA R GCG A CAC	GAT  AGG  R  GAG  GAT  CAC	V 152 AAG K 1206 GCC A GGC G A ATG	TTG L AAC N TAC Y CTT L	GAC D CCT P AGT S TAC Y GCC	107 AAG  K .161 CAG  Q .215 GAG  E	AGA R GAA E ATT I GGT	CGT R GGC GGG GGG	GGC	CGG R TAC Y AAA K ACA T	GAC D AAT N GGC G GCC A GCG GCG	P 1179 GAA E 1233 GAG T ACC T GCC	GAG E CTG L CGC R AAG K	ATG M CAG Q CGGG R GAC ACC	1134 GGG G 1188 AAA  K 1242 AGG  R 1296 ACC  T	2 Chair	
GGA GGC GGC G	GAG E AAG K AAG K AAG K AAG K	.089 GAG  E .143 CCG  P .197 ATG  M	TAC Y AGA R GCG A CAC	GAT  AGG  R  GAG  GAT  CAC	V 152 AAG K 1206 GCC A 260 GGC G	TTG L AAC N TAC Y CTT L	GAC D CCT P AGT S TAC Y GCC	107 AAG K .161 CAG .215 GAG .269 CAG .275	AGA R GAA E ATT I GGT	CGT R GGC GGG GGG	GGC	CGG R TAC Y AAA K ACA T TAA	GAC  AAT  N  GGC  G  GCC  A  GCG  GCG	P 1179 GAA E 1233 GAG T ACC	GAG E CTG R AAG K J GCC	ATG M CAG Q CGGG R GAC	1134 GGG G 1188 AAA  K 1242 AGG  T 1350 GCG	2 Chair	



IL-2 PRODUCTION (O.D.)

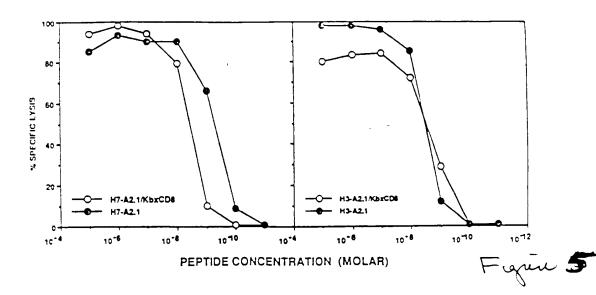


FIGURE 6

•	CCC AAG GCA CTG ATG TTC ATC TTS
√a2	TGA GAC AAA GTC CCC AAT CTC TGA CAG
Vα3 🔖	CTG CAG CTG CTC CTC AAG TAC TAT TC
$V \alpha 4.1.2.3$	TCC CGG AGA AGG TCC ACA GTT CCT CTT T
Vα4 4	GAA GCA GCA GAG GGT TTG AAG CCA CAT AC

2.	•
Va5	GGC AGG TCT TCA GTT GCT TAT GAA GGT
Va6	GGT TCC TCT TCA GGG TCC AGA ATA TGT
Vα7	GCG AAG AAC TCA CCC TGG ACT GTT CAT
Va8	GAG CTC CAC AGA CAA CAA GAG GAC CGA GCA
Vα9	GAG CTG CGA CGT TCC TTA GTG ACT GTG
3	
Val0	CCT CGT CAG CCT GTT GTC CAA TCC TTC TGG
Vall	CA'G CCT CAT CAA TCT GTT CTA CTT GGC T
Vα12	CCA CCA GGG ACC ACA GTT TAT CAT TCA A
Vα14	
Vα15	AGG TCT TGT GTC CCT GAC AGT CCT GGT T
4.	\ \
Val6	CAA GCA AAC ACT GTA GTG CAG AGC CCT TCC
Vα17	CAA GAC ATC CAT AAC TGC CCT ACA G
Val8	GTG TAT GAA ACC CAG GAC AGT TCT TAC
Vα19	CCG TAT TTC TIT CTT ATG TTG TTT TGG AT
Vα20	CAA AGC TCT CCA TCG CTG ACT GTT CAA G
Beta	Groups

• •	1
VB1	ATC TAA TCC TGG GAA GAG CAA AT
Vß2	GGC GTC TGG TAC CAC GTG GTC AA
VB3	GTG AAA GGG CAA GGA CAA AAA GC
VB4	GAT ATG CGA ACÀ GTA TCT AGG C
VB5.1	ACA TAA TCA AAQ GAA AGG GAG AA

2.	\ \ \
VB6	TCC TGA TTG GTC AGG AAG ØGC AA
VB7	TAC CTG ATC AAA AGA ATO GGA GA
VB8.1	ATA ACC ATG ACA ATA TOT ACT GG
VB8.2	ATA ACC ACA ACA ACA TGT ACT GG
VB8.3	ATA GCC ACA ACT ACA/TGT ACT GG
	X
3.	

J.	/ 1
Vβ9	AGC TTG CAA GAG TTG GAA AAC CA
VBIO	GAT TAT GTT TAG CTA CAA TAA TA
VB11	ACA AGG TGA CAG GGA AGG GAC AA
VB12	ACC TAC AGA ACC CAA ÒGA CTC AG
VB13	CAG TTG CCC TCG GAT CGA TTT TC

4.	
VB14	GCC GAG ATC AAG GCT GTG GGC AG
VB15	AGA ACC ATC TGT AAG AGT GGA AC
VB16	CAT CAA ATA ATA GAT ATG GGG CA
Vβ17	GTA GTC CTG AAA AAG GGC ACA CT
Vβ18	CAT CTG TCA AAG TGG CAC TTC A

ange: 1 - 30 odon Table: Universal



on Table : Universal					•sal															
AT	G A						TCC													
Ме	t L	. y <b>s</b>	Ser	Leu	Ser	Val	Ser	Leu	Val	Val	Leu	Trp	Leu	Gln	Leu	Asn	Trp	Val		
CΔ	<b>G</b> Δ	יככ					CAG													

	279				288		297			306				315				
Asp	Gly	Asp	Lys	Lys	Glu	Gly	Arg	Phe	Thr	Ala	His	Leu	Asn	Lys	Ala	Ser	Leu	
GAT		225 GAC																
Trp	Tyr	Arg	Gln	His	Ser	Gly	Glu	Gly	Pro	Lys	Ala	Leu	Met	Ser	Ile	Phe	Ser	
TGG	TAC	171 AGA	CAG	CAT	180 TCT	GGA	GAA	189 GGC	ccc	AAA	198 GCA	CTG	ATG	2 <b>07</b> TCC	ATC	ΤΤÇ	216 TCT	
Gly	Met	Ala	Ser	Leu	Asn								Phe	Gln	Tyr	Phe	Trp	
GGC		117 GCC				TGC	ACT	TCA	AGT	GAT		AAT					162 TGG	
Gln	Ser	Gln	Gln	Lys	Val	Gln	Gln	Ser	Pro	Glu	Ser	Leu	Ser	Val	Pro	Glu	Gly	
CAG	AGC	CAG	CAG	AAG	GTG	CAG	CAG	AGC	CCA	GAA	TCC	CTC	AGT	GTC	CCA	GAG	GGA	

CAT GTT TCC CTG CAC ATC AGA GAC TCC CAG CCC AGT GAC TCC GCT CTC TAC TTC

His Val Ser Leu His Ile Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe

333

342

351

369

378

TGT GCA GTT ATG GAT TAT AAC CAG GGG AAG CTT ATC TTT GGG CAG GGT ACC AAG

Cys Ala Val Met Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys

387 TTA TCT ATC AAG CCC 3'

Leu Ser Ile Lys Pro

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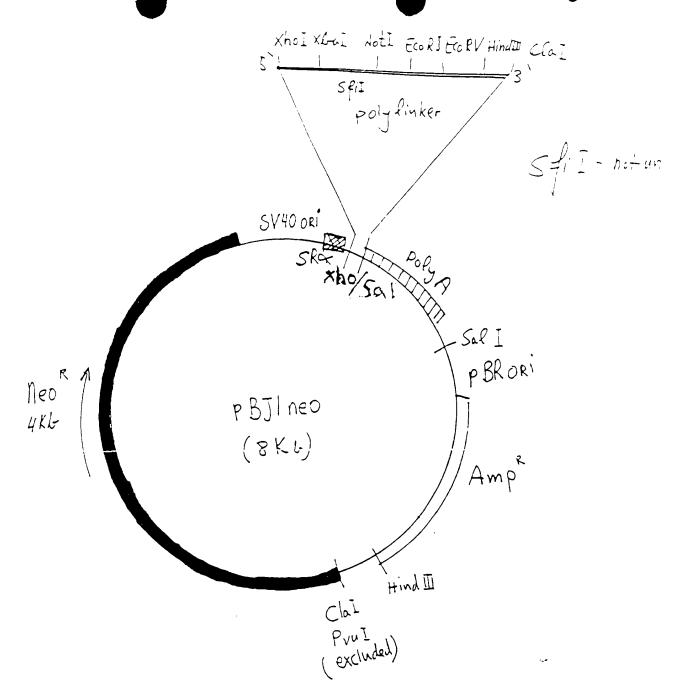
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402 odon Table : Universal

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716 7B

08/8199 18 27 45 36 ATG GGC TCC AGA CTC TTC TTT GTG GTT TTG ATT CTC CTG TGT GCA AAA CAC ATG Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Cys Ala Lys His Met GAG GCT GCA GTC ACC CAA AGT CCA AGA AGC AAG GTG GCA GTA ACA GGA GGA AAG Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val Thr Gly Gly Lys 126 135 144 GTG ACA TTG AGC TGT CAC CAG ACT AAT AAC CAT GAC TAT ATG TAC TGG TAT CGG Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp Tyr Met Tyr Trp Tyr Arq 189 CAG GAC ACG GGG CAT GGG CTG AGG CTG ATC CAT TAC TCA TAT GTC GCT GAC AGC Gln Asp Thr Gly His Gly Leu Arg Leu Ile His Tyr Ser Tyr Val Ala Asp Ser 234 243 ACG GAG AAA GGA GAT ATC CCT GAT GGG TAC AAG GCC TCC AGA CCA AGC CAA GAG Thr Glu Lys Gly Asp Ile Pro Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu 288 **297** 306 AAT TTC TCT CTC ATT CTG GAG TTG GCT TCC CTT TCT CAG TCA GCT GTA TAT TTC Asn Phe Ser Leu Ile Leu Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe 342 351 369 TGT GCC AGC AGC GAT TTC GCC GGG ACA GGG GGC TTC TAT GAA CAG TAC TTC GGT Cys Ala Ser Ser Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly 396 CCC GGC ACC AGG CTC ACG GTT TCT 3' Pro Gly Thr Arg Leu Thr Val Ser



Ref:

pBJI meo - MCB 8: 466, 1988

Polylinker- Science, 249: 677, 1990

